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? e au=martelange valerie

Ref    Items  Index-term
E1         1  AU=MARTELANC E
E2         6  AU=MARTELANGE V
E3         7 *AU=MARTELANGE VALERIE
E4         1  AU=MARTELART A
E5         1  AU=MARTELAT A
E6         1  AU=MARTELE Y
E7         1  AU=MARTELET A
E8        33  AU=MARTELET C
E9        11  AU=MARTELET CLAUDE
E10       10  AU=MARTELET J P
E11        3  AU=MARTELET J-P
E12        1  AU=MARTELET JEAN-PAUL

          Enter P or PAGE for more
? s e2-e3
                6  AU=MARTELANGE V
                7  AU=MARTELANGE VALERIE
      S1       13  E2-E3
? rd
...completed examining records
      S2        7  RD (unique items)
? s s7 and dead
>>>"S7" does not exist
                0  S7
            41760  DEAD
      S3        0  S7 AND DEAD
? s s7 and hage
>>>"S7" does not exist
                0  S7
               48  HAGE
      S4        0  S7 AND HAGE
? t s2/3,ab/all

 2/3,AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10812059   20374312   PMID: 10919659
  Identification  on  a  human sarcoma of two new genes with tumor-specific
expression.
  Martelange V; De Smet C; De Plaen E; Lurquin C; Boon T
  Ludwig  Institute  for  Cancer  Research,  Brussels  Branch, and Cellular
Genetics Unit, Universite Catholique de Louvain, Belgium.
  Cancer research (UNITED STATES)   Jul 15 2000,  60  (14)  p3848-55,
ISSN 0008-5472   Journal Code: 2984705R
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Genes  MAGE,  BAGE,  GAGE, and LAGE-1/NY-ESO-1 code for antigens that are
recognized  on  melanoma  cells  by autologous CTLs. Because the pattern of
expression  of  these  genes  results  in  the presence of antigens on many
tumors  of  various  histological  types  and  not on normal tissues, these
antigens  qualify  for  cancer  immunotherapy.  To  identify new genes with
tumor-specific  expression,  we  applied  a cDNA subtraction approach, ie.,
representational  difference  analysis,  to  a  human sarcoma cell line. We
obtained  two  cDNA  clones  that  appeared  to  be  tumor  specific.  The
corresponding  genes  were  named  SAGE and HAGE because they have the same
pattern  of expression as genes of the MAGE family. SAGE encodes a putative
protein of 904 amino acids and shows no homology to any recorded gene. Like
the  MAGE-A  genes,  it  is  located  in  the  q28  region of chromosome X.
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Expression of gene SAGE was observed mainly in bladder carcinoma, lung carcinoma, and head and neck carcinoma but not in normal tissues, with the exception of testis. Gene HAGE, which is located on chromosome 6, encodes a putative protein of 648 amino acids. This protein is a new member of the DEAD-box family of ATP-dependent RNA helicases. Gene HAGE is expressed in many tumors of various histological types at a level that is 100-fold higher than the level observed in normal tissues except testis. Because of this tumor-specific expression, genes SAGE and HAGE ought to encode antigens that could be useful for antitumoral therapeutic vaccination.

2/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10724809 20281701 PMID: 10820291
High frequency of autologous anti-melanoma CTL directed against an antigen generated by a point mutation in a new helicase gene.
Baurain J F; Colau D; van Baren N; Landry C; **Martelange V**; Vikkula M; Boon T; Coulie P G
Cellular Genetics Unit, Institute of Cellular Pathology, and Laboratory of Human Molecular Genetics, Institute of Cellular Pathology, Universite catholique de Louvain, Brussels, Belgium.
Journal of immunology (Baltimore, Md. : 1950) (UNITED STATES) Jun 1 2000, 164 (11) p6057-66, ISSN 0022-1767 Journal Code: 2985117R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
We have identified an Ag recognized by autologous CTL on the melanoma cells of a patient who enjoyed an unusually favorable clinical evolution. The antigenic peptide, which is presented by HLA-A28 molecules, is encoded by a mutated sequence in a new gene. This gene, which was named MUM-3, is expressed ubiquitously and shows homology with the RNA helicase gene family. Limiting dilution analysis indicated that at least 0.15% of the blood CD8 T cells were tumor-specific CTL precursors. The MUM-3 Ag was recognized by 90% of these CTL, indicating that it is the dominant target Ag of the tumor-specific CTL response. The high frequency of anti-MUM-3 CTL was confirmed with tetramers of soluble HLA-A28 molecules loaded with the antigenic peptide. MUM-3 tetramers stained 1.2% of blood CD8 cells, a frequency that has never been reported for T cells directed against a strictly tumor-specific Ag. To confirm these results, the CD8 T cells that were clearly labeled with tetramers were restimulated in clonal conditions. About 90% of these cells proliferated, and all the resulting clones proved lytic and MUM-3 specific. By improving the conditions used for the in vitro restimulation of CTL precursors by the tumor cells, the same frequency could be obtained in limiting dilution analysis. These results show that some cancer patients have a high frequency of circulating CTL that are directed against a strictly tumor-specific Ag. These CTL are responsive to restimulation in vitro and are easily detected with tetramers. Such responses may therefore be an achievable goal for therapeutic vaccination with tumor-specific Ags.

2/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10459140 99454989 PMID: 10523621
DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.
De Smet C; Lurquin C; Lethe B; **Martelange V**; Boon T
Ludwig Institute for Cancer Research, Brussels Branch, Brussels B-1200, Belgium.
Molecular and cellular biology (UNITED STATES) Nov 1999, 19 (11) p7327-35, ISSN 0270-7306 Journal Code: 8109087

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

A subset of male germ line-specific genes, the MAGE-type genes, are activated in many human tumors, where they produce tumor-specific antigens recognized by cytolytic T lymphocytes. Previous studies on gene MAGE-A1 indicated that transcription factors regulating its expression are present in all tumor cell lines whether or not they express the gene. The analysis of two CpG sites located in the promoter showed a strong correlation between expression and demethylation. It was also shown that MAGE-A1 transcription was induced in cell cultures treated with demethylating agent 5'-aza-2'-deoxycytidine. We have now analyzed all of the CpG sites within the 5' region of MAGE-A1 and show that for all of them, demethylation correlates with the transcription of the gene. We also show that the induction of MAGE-A1 with 5'-aza-2'-deoxycytidine is stable and that in all the cell clones it correlates with demethylation, indicating that demethylation is necessary and sufficient to produce expression. Conversely, transfection experiments with in vitro-methylated MAGE-A1 sequences indicated that heavy methylation suffices to stably repress the gene in cells containing the transcription factors required for expression. Most MAGE-type genes were found to have promoters with a high CpG content. Remarkably, although CpG-rich promoters are classically unmethylated in all normal tissues, those of MAGE-A1 and LAGE-1 were highly methylated in somatic tissues. In contrast, they were largely unmethylated in male germ cells. We conclude that MAGE-type genes belong to a unique subset of germ line-specific genes that use DNA methylation as a primary silencing mechanism.

2/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10179705 99134295 PMID: 9933564

A new family of mouse genes homologous to the human MAGE genes.

De Plaen E; De Backer O; Arnaud D; Bonjean B; Chomez P; **Martelange V**; Avner P; Baldacci P; Babinet C; Hwang S Y; Knowles B; Boon T

Brussels Branch, 74 avenue Hippocrate-UCL 74.59, Brussels, B1200, Belgium.

Genomics (UNITED STATES) Jan 15 1999, 55 (2) p176-84, ISSN 0888-7543 Journal Code: 8800135

Contract/Grant No.: USPHS 35252; SP; CSAP

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The human MAGE genes are expressed in a wide variety of tumors but not in normal cells, with the exception of the male germ cells, placenta, and, possibly, cells of the developing embryo. These genes encode tumor-specific antigens recognized by cytolytic T lymphocytes. The MAGE genes are located on the X chromosome, in three clusters denoted MAGE-A, B, and C, mapping at q28, p21.3, and q26, respectively. The function of these genes remains unknown. Because mice offer many advantages for the study of genes that may be involved in embryonic development, we looked for the murine equivalents of the 12 human MAGE-A genes. Using a MAGE-A probe, we isolated 8 new murine genes that are homologous to the MAGE genes. On average, the open reading frames (ORFs) of these 8 closely related genes display a slightly higher degree of nucleotide identity with the MAGE-A ORFs than with the MAGE-B or MAGE-C ORFs. Furthermore, like MAGE-A genes, they encode acidic proteins, whereas the MAGE-B genes encode basic proteins. Accordingly, these 8 murine genes were named Mage-a1 to 8 (approved symbols Magea1 to 8). Mage-a genes were mapped in two different loci on the mouse X chromosome. Mage-a4 and Mage-a7 are located in a region that is syntenic to either Xp21 or Xq28. The 6 other genes are arranged in a cluster located in

a region syntenic to Xp22. Like their human counterparts, Mage-a genes were found to be transcribed in adult testis, but not in other tissues. Expression of some Mage-a genes was also detected in tumor cell lines. Two Mage-a genes were found to be expressed in blastocysts. Copyright 1999 Academic Press.

2/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09692763 98110575 PMID: 9441743
Two members of the human MAGEB gene family located in Xp21.3 are expressed in tumors of various histological origins.
Lurquin C; De Smet C; Brasseur F; Muscatelli F; **Martelange V**; De Plaen E; Brasseur R; Monaco A P; Boon T
Ludwig Institute for Cancer Research, Brussels Branch, Belgium. lurquin@licr.ucl.ac.be
Genomics (UNITED STATES) Dec 15 1997, 46 (3) p397-408, ISSN 0888-7543 Journal Code: 8800135
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Genes of the MAGE family direct the expression of tumor antigens recognized on a human melanoma by autologous cytolytic T lymphocytes. Twelve closely related MAGE genes are located in the Xq28 region. These genes share 60-98% nucleotide identity in their coding region. The presence of homologous genes in a region of Xp21.3 has been reported previously. We obtained the complete sequence of a 42-kb stretch of this region. It contains four MAGE-related genes, which we propose to name MAGE-B1, B2, B3, and B4 (HGMW-approved symbols MAGEB1, MAGEB2, MAGEB3, and MAGEB4). The coding regions of these genes share 66-81% nucleotide identity and show 45-63% identity with those of the MAGE genes located in Xq28. Like the MAGE genes located in Xq28, the MAGE-B genes are silent in normal tissues with the exception of testis. Like MAGE-1, 2, 3, 4, 6 and 12 (HGMW-approved symbols MAGEA1, 2, 3, 4, 6, and 12), genes MAGE-B1 and MAGE-B2 are expressed in a significant fraction of tumors of various histological types. The transcription of MAGE-B1 and MAGE-B2 can be induced by 5-aza-2'-deoxycytidine, suggesting that the activation of these genes in tumors results from a demethylation process.

2/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09675428 98096376 PMID: 9434763
Identification of human testis-specific transcripts and analysis of their expression in tumor cells.
De Smet C; **Martelange V**; Lucas S; Brasseur F; Lurquin C; Boon T
Ludwig Institute for Cancer Research, Brussels, Belgium.
Biochemical and biophysical research communications (UNITED STATES) Dec 29 1997, 241 (3) p653-7, ISSN 0006-291X Journal Code: 0372516
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Tumor-specific antigens recognized by autologous T lymphocytes are encoded by genes, including those of the MAGE, BAGE, and GAGE gene families, that are expressed in a significant fraction of tumors of various types, but not in normal adult tissues, except for testis where they appear to be expressed in germ cells. Because male germ cells are known to express many genes that are not expressed in other normal adult tissues, we wished to determine whether most of these genes are occasionally activated in tumor cells. Representational difference analysis was used to obtain

testis-specific transcripts. The expression of 15 testis-specific cDNA sequences was tested by RT-PCR in a series of tumor cell lines. Only one cDNA sequence showed a significant level of expression in some tumor cell lines. Remarkably, this cDNA clone proved to be a new gene of the MAGE family. These results suggest that MAGE, BAGE, and GAGE genes belong to a minor subset of testis-specific genes that is often activated in tumors of various types, whereas most testis-specific genes are either never or very rarely activated in tumors.

2/3,AB/7 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13377215 BIOSIS NO.: 200200006036
Tumor associated nucleic acids and uses therefor.
AUTHOR: **Martelange Valerie**(a); De Smet Charles; Boon-Falleur Thierry
AUTHOR ADDRESS: (a)Brussels**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office Patents 1251 (3):pNo Pagination Oct. 16, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The invention describes sdp3.8 tumor associated nucleic acids, including fragments and biologically functional variants thereof. Also included are polypeptides and fragments thereof encoded by such nucleic acids, and antibodies relating thereto. Methods and products also are provided for diagnosing and treating conditions characterized by expression of a sdp3.8 gene product.

2001

2001
? s hage
      S5   48 HAGE
? s s5 and tumor?
               48 S5
          1221572 TUMOR?
      S6   6 S5 AND TUMOR?
? rd
...completed examining records
      S7   5 RD (unique items)
? t s7/3,ab/all

 7/3,AB/1   (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

13007969   21929228   PMID: 11931711
  Immunomodulatory activity of orphanin FQ/nociceptin on traumatic rats.
  Zhao Hui; Wu Gen-Cheng; Cao Xiao-Ding
  National Key Laboratory of Medical Neurobiology, Department of Neurobiology, Medical College of Fudan University, Shanghai 200032, China. cdcao@shmu.edu.cn
  Acta pharmacologica Sinica (China) Apr 2002, 23 (4) p343-8, ISSN 1671-4083 Journal Code: 100956087
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: In Process
  AIM: To explore the neuro-immune modulatory effect of orphanin FQ/nocic eptin (OFQ) and opioid receptor like 1 (ORL1) receptor on the traumatic rats. METHODS: The quantitative method of immuno-cytochemistry and i n situ hybridization combined with cytokine bioassay were used to detect the expression of endogenous OFQ and ORL1 and the production of interleukin-1 (IL-1) and **tumor** necrosis factor-alpha (TNF-alpha) from perit oneal macrophage. RESULTS: Strong signals for both OFQ immuno-reactive cells and O RL1 mRNA were detected in cerebral cortex, hippocampus, and hypothalamus in normal condition, whereas they were significantly reduced after trauma (P<0.05). However, the production of IL-1 and TNF-alpha from peritoneal macrop **hage** was increased, when expressed as percentage of enhancement, the increment attained to 233 % and 521 % (sample dilution 1:4), 195 % and 566 % (1:8), 233 % and 757 % (1:16), 214 % and 622 % (1:32), respectively, after trauma. After icv injec tion of OFQ at doses of 0.055 nmol, 0.55 nmol, and 2.75 nmol, the units of IL-1 and TNF-alpha were reversed (P<0.05); however, the action of OFQ (0.55 nmol) was blocked by ORL1 selective antagonist [phe1 (CH2-NH)Gly2]nociceptin-(1-13)-NH2. CONCLUSION: OFQ and ORL1, the new opioid peptide system, are invo lved in the immune response elicited by traumatic stress.

 7/3,AB/2   (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10812059   20374312   PMID: 10919659
   Identification on a human sarcoma of two new genes with **tumor** -specific expression.
  Martelange V; De Smet C; De Plaen E; Lurquin C; Boon T
  Ludwig Institute for Cancer Research, Brussels Branch, and Cellular Genetics Unit, Universite Catholique de Louvain, Belgium.
  Cancer research (UNITED STATES) Jul 15 2000, 60 (14) p3848-55, ISSN 0008-5472 Journal Code: 2984705R
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Genes MAGE, BAGE, GAGE, and LAGE-1/NY-ESO-1 code for antigens that are

recognized on melanoma cells by autologous CTLs. Because the pattern of expression of these genes results in the presence of antigens on many **tumors** of various histological types and not on normal tissues, these antigens qualify for cancer immunotherapy. To identify new genes with **tumor** -specific expression, we applied a cDNA subtraction approach, ie., representational difference analysis, to a human sarcoma cell line. We obtained two cDNA clones that appeared to be **tumor** specific. The corresponding genes were named SAGE and **HAGE** because they have the same pattern of expression as genes of the MAGE family. SAGE encodes a putative protein of 904 amino acids and shows no homology to any recorded gene. Like the MAGE-A genes, it is located in the q28 region of chromosome X. Expression of gene SAGE was observed mainly in bladder carcinoma, lung carcinoma, and head and neck carcinoma but not in normal tissues, with the exception of testis. Gene **HAGE**, which is located on chromosome 6, encodes a putative protein of 648 amino acids. This protein is a new member of the DEAD-box family of ATP-dependent RNA helicases. Gene **HAGE** is expressed in many **tumors** of various histological types at a level that is 100-fold higher than the level observed in normal tissues except testis. Because of this **tumor**-specific expression, genes SAGE and **HAGE** ought to encode antigens that could be useful for antitumoral therapeutic vaccination.

7/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03142377 79184132 PMID: 87088
Does the cancer accompanying acanthosis nigricans contain endocrine cells of the APUD series?
Curth H O
Acta dermato-venereologica (SWEDEN) 1979, 59 (3) p261-3, ISSN 0001-5555 Journal Code: 0370310
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Following the publication of **Hage** & **Hage**, who believe that gastric cancers accompanying malignant acanthosis nigricans might constitute a specific group of carcinomas in which cells from parts of the **tumor** arise from the APUD-series of endocrine cells, carcinomas of 2 patients with malignant acanthosis nigricans were subjected to investigation. There were no APUD-cells in the adenocarcinomas studied but they were present in the overlying mucosa. It is known, moreover, that internal carcinomas not accompanying malignant acanthosis nigricans may contain APUD cells.

7/3,AB/4 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

13198981 BIOSIS NO.: 200100406130
Expression of tumour-associated antigens in presentation myeloid leukaemias.
AUTHOR: Adams Stuart P(a); Guinn Barbara A(a); Mijovic Aleksandar(a); Czepulkowski Barbara(a); Mufti Ghulam J(a)
AUTHOR ADDRESS: (a)Leukaemia Sciences, Guy's, King's and St. Thomas' School of Medicine, Rayne Institute, London, SE5 9NU**UK
JOURNAL: British Journal of Haematology 113 (Supplement 1):p26 May, 2001
MEDIUM: print
CONFERENCE/MEETING: Annual Scientific Meeting of the British Society for Haematology Harrogate, England, UK April 23-26, 2001
ISSN: 0007-1048
RECORD TYPE: Citation

LANGUAGE: English
SUMMARY LANGUAGE: English
2001

7/3,AB/5 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

02725388 BIOSIS NO.: 000068035986
ULTRASTRUCTURAL AND HISTOLOGICAL STUDY OF 11 BRONCHIAL CARCINOIDS EVIDENCE FOR DIFFERENT TYPES
AUTHOR: CAPELLA C; GABRIELLI M; POLAK J M; BUFFA R; SOLCIA E; BORDI C
AUTHOR ADDRESS: CENT. DIAGN. ISTOPATHOL., OSP. CIRCOLO, UNIV. PAVIA, VIALE L. BORRI 57, I-21100 VARESE, ITALY.
JOURNAL: VIRCHOWS ARCH A PATHOL ANAT HISTOL 381 (3). 1979. 313-330. 1979
CODEN: VAAPB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Seven of 11 bronchial carcinoids investigated showed cells with small granules resembling P [pleural] cells which have already been described in human fetal and adult lung; 2 of these P cell **tumors** showed distinctive paraganglioid features. One **tumor** showed peculiar ultrastructural findings resembling closely those previously reported by Black in a so called "pulmonary oncocytoma". Three remaining cases showed large secretory granules resembling those of type 3 cells already described by **Hage** in bronchial carcinoids; 1 of these **tumors** produced large amounts of 5-hydroxytryptamine (5HT). On cytological grounds, at least 2 types of **tumors** can be distinguished among bronchial carcinoids, i.e., P cell and type 3 cell **tumors**. Two varieties of P cell carcinoids have been recognized, showing either the less frequent and more distinctive paraganglioid structure or the more common trabecular structure.

1979